

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2003, 16:23:48 ; Search time 40.4571 Seconds
(without alignments)
102.055 Million cell updates/sec

Title: US-09-905-691-5

Perfect score: 16

Sequence: 1 CRRARAARARAE 16

Scoring table: OLIGO

Gapop 60.0 , Gapert 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	56.2	105	2 P96802	P96802 mycobacteri
2	9	56.2	105	16 Q9CCQ8	Q9CCQ8 mycobacteri
3	9	56.2	190	16 P71658	P71658 mycobacteri
4	9	56.2	406	10 Q94EV7	Q94EV7 zea mays (m
5	9	56.2	750	16 Q9KXP6	Q9KXP6 streptomyce
6	8	50.0	101	11 Q8BMV6	Q8BMV6 mus musculu
7	8	50.0	167	10 Q8SLJ9	Q8SLJ9 oryza sativ
8	8	50.0	200	2 Q9X696	Q9X696 streptomyce
9	8	50.0	204	12 Q85545	Q85545 bovine herp
10	8	50.0	274	10 Q8G2E4	Q8G2E4 pyrocystis
11	8	50.0	336	2 Q9X4X0	Q9X4X0 pseudomonas
12	8	50.0	356	7 Q31191	Q31191 mus musculu
13	8	50.0	383	16 Q914A1	Q914A1 pseudomonas
14	8	50.0	451	10 Q8S1I2	Q8S1I2 oryza sativ
15	8	50.0	710	16 Q8YER0	Q8YER0 brucella me
16	8	50.0	820	16 Q98C41	Q98C41 rhizobium l

17	8	50.0	897	5	O60961	O60961 leishmania
18	8	50.0	998	16	Q9S2K3	Q9S2K3 streptomyce
19	7	43.8	69	16	Q8YUB7	Q8YUB7 anabaena sp
20	7	43.8	77	16	Q8Z368	Q8Z368 salmonella
21	7	43.8	79	16	Q8FJ33	Q8FJ33 escherichia
22	7	43.8	109	12	O11376	O11376 molluscum c
23	7	43.8	110	12	Q98316	Q98316 molluscum c
24	7	43.8	112	10	Q8H286	Q8H286 ananas como
25	7	43.8	126	16	Q8KB34	Q8KB34 chlorobium
26	7	43.8	132	16	Q8P9A4	Q8P9A4 xanthomonas
27	7	43.8	157	4	Q8N9D2	Q8N9D2 homo sapien
28	7	43.8	159	16	Q910C1	Q910C1 pseudomonas
29	7	43.8	161	4	Q8NH35	Q8NH35 homo sapien
30	7	43.8	174	16	Q9A3B0	Q9A3B0 caulobacter
31	7	43.8	178	10	Q8LHL2	Q8LHL2 oryza sativ
32	7	43.8	184	16	Q8FS32	Q8FS32 corynebacte
33	7	43.8	188	2	Q9R6M4	Q9R6M4 agrobacteri
34	7	43.8	193	4	Q8WY44	Q8WY44 homo sapien
35	7	43.8	204	5	Q9U6W9	Q9U6W9 manduca sex
36	7	43.8	206	16	Q8PK00	Q8PK00 xanthomonas
37	7	43.8	210	11	Q9D6J8	Q9D6J8 mus musculu
38	7	43.8	212	12	O11344	O11344 molluscum c
39	7	43.8	227	16	Q8PRF8	Q8PRF8 xanthomonas
40	7	43.8	232	16	Q8XRJ0	Q8XRJ0 raietonia s
41	7	43.8	234	16	Q8FW01	Q8FW01 brucella su
42	7	43.8	251	10	Q8S6W0	Q8S6W0 oryza sativ
43	7	43.8	252	16	Q8YBM6	Q8YBM6 brucella me
44	7	43.8	264	10	Q94J70	Q94J70 oryza sativ
45	7	43.8	276	16	Q8NRM1	Q8NRM1 corynebacte

ALIGNMENTS

RESULT 1

P96802 PRELIMINARY; PRT; 105 AA.
AC P96802;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Integration host factor.
OS MIHF.
GN Mycobacterium smegmatis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1772;
RN [1]
RP SEQUENCE FROM N.A.
RA Pedulla M.L., Lee M.H., Lever D.C., Hatfull G.F.;
RT "A novel host factor for integration of mycobacteriophage L5.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75344; AAC28246.1; -;
SQ SEQUENCE 105 AA; 11635 MW; B73846DBFA6CA838 CRC64;

Query Match 56.2%; Score 9; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARAE 15
|||||

Db 19 AAARRARAE 27

RESULT 2

Q9CCQ8 PRELIMINARY; PRT; 105 AA.
AC Q9CCQ8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Putative integration host factor.
GN MIHF OR ML0540.

OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.N., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus";
 RL Nature 409:1007-1011(2001).
 DR EMBL; AL583918; CAC30048.1; -.
 DR Leproma; ML0540; -.
 KW Complete proteome.
 SQ SEQUENCE 105 AA; 11506 MW; BDCD218AEFF76238 CRC64;

Query Match 56.2%; Score 9; DB 16; Length 105;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARAE 15
 Db | | | | | | | | | |
 19 AAARRARAE 27

RESULT 3

ID P71658 PRELIMINARY; PRT; 190 AA.
 AC P71658;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein RV1388.
 GN RV1388 OR M71433 OR M7C21B4.05.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37Rv;
 RX MEDLINE=98235987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG, TO M.SMEGMATIS MIHF.

DR EMBL; Z80108; CAB02193.1; -.
 DR EMBL; AE007015; AKA45698.1; ALT_INIT.
 DR TIGR; M71433; -.
 DR Tubercultist; RV1388; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 190 AA; 20835 MW; 376672DCF96AF60D CRC64;

Query Match 56.2%; Score 9; DB 16; Length 190;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARAE 15
 Db | | | | | | | | | |
 104 AAARRARAE 112

RESULT 4

Q94EV7
 ID Q94EV7 PRELIMINARY; PRT; 406 AA.
 AC Q94EV7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE MAP kinase kinase.
 GN MAPKK1.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON-Huck1;
 RA Fu H., Zheng Z., Dooner H.K.;
 RT "Large differences in recombination rates within adjacent gene-dense
 and retrotransposon regions of maize";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AF391808; AAK73104.1; -.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002965; P-rich_extensn.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR01217; PRICHEXTENS.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 406 AA; 44664 MW; DBFIDE6368F47DF0 CRC64;

Query Match 56.2%; Score 9; DB 10; Length 406;
 Best Local Similarity 100.0%; Pred. No. 8.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAARRAAR 10
 Db | | | | | | | | | |
 72 RRAARRAAR 80

RESULT 5

Q9KXP6
 ID Q9KXP6 PRELIMINARY; PRT; 750 AA.
 AC Q9KXP6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein SCO1504.
 GN SCO1504 OR SC9C5.28.
 OS Streptomyces coelicolor.

Sat Aug 9 19:18:32 2003

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;
 RN SEQUENCE FROM N.A.

RP STRAIN-A3(2);

RA Brown S.P., Harris D.;

RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RP STRAIN-A3(2);

RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;

RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RP STRAIN-A3(2);

RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,

RA Kinashi H., Hopwood D.A.; and a detailed genetic and physical map for

RT "A set of ordered cosmids and a detailed genetic and physical map for

RL the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

RN Mol. Microbiol. 21:77-96(1996).

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2)/M145;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,

RA Rabbinkowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;

RP "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2).";

RL Nature 417:141-147(2002).

DR EMBL; AL939109; CAB93384.1; -

DR InterPro; IPR000767; Disease_Resist.

DR PRINTS; PR00364; DISEASESIST.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 750 AA; 81839 MW; 469E5F417EDC8862 CRC64;

Query Match 56.28; Score 9; DB 16; Length 750;

Best Local Similarity 100.0%; Pred. No. 14; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0;

QY 4 AAAAAA 12

DB 76 AAAAAA 84

RESULT 6

Q8BMV6 PRELIMINARY; PRT; 101 AA.

AC Q8BMV6;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical type I antifreeze protein containing protein

DE (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.

RP STRAIN-C57BL/6J; TISSUE-Eye;

RX MEDLINE-22354683; PubMed-12466851;

RA THE FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.*;
 RL Nature 420:563-573(2002).
 DR EMBL; AK021392; BAC25654.1;
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 101 AA; 10110 MW; CBDCDC2D530ABB15 CRC64;

Query Match 50.08; Score 8; DB 11; Length 101;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAARAAAR 10

DB 67 RAARAAAR 74

RESULT 7

Q8SLJ9 PRELIMINARY; PRT; 167 AA.

AC Q8SLJ9;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE P0684C02.19 protein.

DE P0684C02.19.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=39947;

RN SEQUENCE FROM N.A.

RC STRAIN-cv. Nipponbare;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC

clone: P0684C02.19";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP003290; BAB89063.1;

DR Gramene; Q8SLJ9;

SQ SEQUENCE 167 AA; 18542 MW; 0C40040DFB49021B CRC64;

Query Match 50.08; Score 8; DB 10; Length 167;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRAARAAA 9

DB 20 RRAARAAA 27

RESULT 8

Q9X696 PRELIMINARY; PRT; 200 AA.

AC Q9X696;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Vdcb.

DE Vdcb.

GN Vdcb.

OS Streptomyces sp. (strain D7).

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=92742;

RN SEQUENCE FROM N.A.

RP STRAIN-D7;

RC STRAIN-D7;

RX Chow K.T., Pope M.K., Davies J.;

RT "Characterization of a vanillic acid non-oxidative decarboxylation

gene cluster from Streptomyces sp. D7.";

RL Microbiology 145:2393-2403(1999).

DR EMBL; AF134589; AAD28781.1;

DR InterPro; IPR003382; Flavoprotein.

DR InterPro: IPR004507; Ublx.
DR Pfam: PF02441; Flavoprotein: 1.
DR TIGRFAMs: TIGR00421; ublx: 1.
SQ SEQUENCE 200 AA; 21660 MW; 83D1B5C22C13CD3E CRC64;

Query Match 50.0%; Score 8; DB 10; Length 274;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARA 14
| | | | | | | |
DB 81 AAARRARA 88

RESULT 11
Q9X4X0 PRELIMINARY; PRT; 336 AA.
AC Q9X4X0;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE DITH.
GN DITH.
OS Pseudomonas abietaniphila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=89065;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KME-9;
RA Mohn W.W., Wilson A.E., Bicho P., Moore E.R.B.;
RT "Physiological and Phylogenetic Diversity of Bacteria Growing on Resin Acids";
RL Syst. Appl. Microbiol. 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KME-9;
RX MEDLINE=99235742; PubMed=10217753;
RA Martin V.J., Mohn W.W.;
RT "A novel aromatic-ring-hydroxylating dioxygenase from the diterpenoid-degrading bacterium Pseudomonas abietaniphila KME-9";
RL J. Bacteriol. 181:2675-2682(1999).
DR ENBL: AF119621; AAD21070.1;
DR InterPro: IPR002529; FAA_hydrolase.
DR Pfam: PF01557; FAA_hydrolase; 1.
SQ SEQUENCE 336 AA; 37494 MW; CD221163FB1B44FB CRC64;

Query Match 50.0%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAARRARA 14
| | | | | | | |
DB 105 AAARRARA 112

RESULT 12
Q31191 PRELIMINARY; PRT; 356 AA.
AC Q31191;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE MHC class I H2-K gene (Haplotype d) (fragment).
GN H2-K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84170268; PubMed=6143316;
RA Lalanne J.-L., Cochet M., Kummer A.-M., Gachelin G., Kourilsky P.;
RT "Different exon-intron organization at the 5' part of a mouse class I gene is used to generate a novel H-2Kd-related mRNA";
RL Proc. Natl. Acad. Sci. U.S.A. 80:7561-7565(1983).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM (BY SIMILARITY).

DR InterPro: IPR004507; Ublx.
DR Pfam: PF02441; Flavoprotein: 1.
DR TIGRFAMs: TIGR00421; ublx: 1.
SQ SEQUENCE 200 AA; 21660 MW; 83D1B5C22C13CD3E CRC64;

Query Match 50.0%; Score 8; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAARAAAR 10
| | | | | | | |
DB 187 RAARAAAR 194

RESULT 9
Q65545 PRELIMINARY; PRT; 204 AA.
AC Q65545;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE UL3 protein.
GN UL3.
OS Bovine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cooper;
RX MEDLINE=96036477; PubMed=7483276;
RA Khattar S.K., van Drunen Littel-van den Hurk S., Babiuk L.A.,
RA Tikoo S.K.;
RT "Identification and transcriptional analysis of a 3'-coterminial gene cluster containing UL1, UL2, UL3, and UL3.5 open reading frames of bovine herpesvirus-1";
RL Virology 213:28-37(1999).
DR ENBL: U32173; AAC54557.1;
DR InterPro: IPR005035; Herpes_UL3.
DR InterPro: IPR005829; Sug. transporter.
DR Pfam: PF03369; Herpes_UL3; 1.
DR PROSITE: PS00216; SUGAR_TRANSPORT_1; 1.
SQ SEQUENCE 204 AA; 21792 MW; 9292E6A8AA2CB8C6 CRC64;

Query Match 50.0%; Score 8; DB 12; Length 204;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAARAAAR 10
| | | | | | | |
DB 113 RAARAAAR 120

RESULT 10
Q8G2E4 PRELIMINARY; PRT; 274 AA.
AC Q8G2E4;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Chlorophyll A-C binding protein.
OS Pyrocystis lunula.
OC Eukaryota; Alveolata; Dinophyceae; Pyrocystales; Pyrocystis.
OX NCBI_TaxID=2972;
RN [1]
RP SEQUENCE FROM N.A.
RX Okamoto O.K., Hastings J.W.;
RT "Circadian oscillations in the transcriptome of dinoflagellate cells: Towards the clock circuitry";
RL Submitted (Apr-2002) to the ENBL/GenBank/DBJ databases.
DR ENBL: AF508261; AAO14680.1;
SQ SEQUENCE 274 AA; 28168 MW; B5F52A5D45AC8BA CRC64;

CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN) (BY SIMILARITY).

DR EMBL; K01182; AAA39653.1; -
 DR HSP; P01899; I829.
 DR MGD; MGI:95904; H2-K.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR001039; MHC_I.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00129; MHC_I; 1.
 DR PRINTS; PR01638; MHCCLASSI.
 DR ProDom; PD000050; MHC_I; 1.
 DR SMART; SM00407; IGC1; 1.
 DR PROSITE; PS08335; Ig_LIKE; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Glycoprotein; Transmembrane.
 FT NON_TER 356 356
 SQ SEQUENCE 356 AA; 39888 MW; 7BFB4957212E3F2D CRC64;

Query Match 50.0%; Score 8; DB 7; Length 356;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ARAAAR 10
 DB 20 ARAAAR 27
 |||||||

RESULT 13

OYI4A1 PRELIMINARY; PRT; 383 AA.
 AC OYI4A1;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Probable multidrug resistance efflux pump.
 GN PA1237.

OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PAOI;
 RX MEDLINE-20437337; PubMed-10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
 RT opportunistic pathogen";
 RL Nature 405:959-964(2000).
 DR EMBL; AF004533; ANG04626.1; -
 DR InterPro; IPR006143; HlyD.
 DR InterPro; IPR003997; RTX.
 DR Pfam; PF00529; HlyD; 1.
 DR PRINTS; PR01490; RTXTOXIND.
 KW Complete proteome.

SQ SEQUENCE 383 AA; 42550 MW; 8DE3B490DD83C9B1 CRC64;
 Query Match 50.0%; Score 8; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 ARAAAR 12
 DB 187 ARAAAR 194
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RESULT 14

Q8S112

ID Q8S112 PRELIMINARY; PRT; 451 AA.
 AC Q8S112;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE P0699H05.2 protein.
 GN P0699H05.2.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone: P0699H05.2";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003299; BAB9880.1; -
 DR Gramene; Q8S112; -
 SQ SEQUENCE 451 AA; 49641 MW; 2E196EAAIDCB1468 CRC64;

Query Match 50.0%; Score 8; DB 10; Length 451;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RRAAAR 9
 DB 237 RRAAAR 244
 |||||||

RESULT 15

OYI818 PRELIMINARY; PRT; 710 AA.
 AC OYI818;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ATP-dependent helicase HRPB.
 GN BMEI1818.

OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-16M / ATCC 23456 / Biotype 1;
 RX MEDLINE-20020109; PubMed-11756688;
 RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mueh C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009614; AAL52999.1; -
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICC; 1.
 KW Complete proteome.

SQ SEQUENCE 710 AA; 76150 MW; 5DCA5720C36DBBFA CRC64;
 Query Match 50.0%; Score 8; DB 16; Length 710;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ARAAAR 11
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Db 156 AAAAAARR 163

Search completed: August 9, 2003, 16:32:58
Job time : 40.4571 secs